

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/175,713DATE: 11/03/98  
TIME: 15:35:12

INPUT SET: S29599.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Herrmann, Stephen H.  
6 Lu, Zhijian  
7 McCoy, John M.  
8 Swanberg, Stephen L.  
9 Walker, Bruce  
10 Yang, Otto  
11  
12 (ii) TITLE OF INVENTION: CHEMOKINES WITH AMINO-TERMINAL MODIFICATIONS  
13  
14 (iii) NUMBER OF SEQUENCES: 15  
15  
16 (iv) CORRESPONDENCE ADDRESS:  
17 (A) ADDRESSEE: Genetics Institute, Inc.  
18 (B) STREET: 87 CambridgePark Drive  
19 (C) CITY: Cambridge  
20 (D) STATE: MA  
21 (E) COUNTRY: U.S.A.  
22 (F) ZIP: 02140  
23  
24 (v) COMPUTER READABLE FORM:  
25 (A) MEDIUM TYPE: Floppy disk  
26 (B) COMPUTER: IBM PC compatible  
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
29  
30 (vi) CURRENT APPLICATION DATA:  
31 (A) APPLICATION NUMBER:  
32 (B) FILING DATE:  
33 (C) CLASSIFICATION:  
34  
35 (viii) ATTORNEY/AGENT INFORMATION:  
36 (A) NAME: Sprunger, Suzanne A.  
37 (B) REGISTRATION NUMBER: 41,323  
38  
39 (ix) TELECOMMUNICATION INFORMATION:  
40 (A) TELEPHONE: (617) 498-8284  
41 (B) TELEFAX: (617) 876-5851  
42  
43  
44 (2) INFORMATION FOR SEQ ID NO:1:  
45  
46 (i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 89 amino acids  
48 (B) TYPE: amino acid  
49 (C) STRANDEDNESS:  
50 (D) TOPOLOGY: linear  
51

52 (ii) MOLECULE TYPE: protein  
53  
54  
55  
56

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
58

59 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu  
60 1 5 10 15  
61

62 Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys  
63 20 25 30  
64

65 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys  
66 35 40 45  
67

68 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys  
69 50 55 60  
70

71 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
72 65 70 75 80  
73

74 Glu Tyr Leu Glu Lys Ala Leu Asn Lys  
75 85  
76

77 (2) INFORMATION FOR SEQ ID NO:2:  
78

79 (i) SEQUENCE CHARACTERISTICS:  
80 (A) LENGTH: 93 amino acids  
81 (B) TYPE: amino acid  
82 (C) STRANDEDNESS:  
83 (D) TOPOLOGY: linear  
84

85 (ii) MOLECULE TYPE: protein  
86  
87  
88  
89

90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
91

92 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu  
93 1 5 10 15  
94

95 Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys  
96 20 25 30  
97

98 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys  
99 35 40 45

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100  
101 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys  
102 50 55 60  
103  
104 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
105 65 70 75 80  
106  
107 Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met  
108 85 90  
109

110 (2) INFORMATION FOR SEQ ID NO:3:

111 (i) SEQUENCE CHARACTERISTICS:

112 (A) LENGTH: 1856 base pairs

113 (B) TYPE: nucleic acid

114 (C) STRANDEDNESS: double

115 (D) TOPOLOGY: linear

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117 (ii) MOLECULE TYPE: cDNA

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123 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

124

125 TCTCCGTCAG CCGCATTGCC CGCTCGGCGT CCGGCCCCCG ACCCGTGCTC GTCCGCCCCG 60

126 CCGCCCCGCC GCGCGGCCA TGAACGCCAA GGTCGTGGTC GTGCTGGTCC TCGTGCTGAC 120

127 CGCGCTCTGC CTCAGCGACG GGAAGCCCGT CAGCCTGAGC TACAGATGCC CATGCCGATT 180

128 CTTCGAAAGC CATGTTGCCA GAGCCAACGT CAAGCATCTC AAAATTCTCA AACTCCAAA 240

129 CTGTGCCCTT CAGATTGTAG CCCGGCTGAA GAACAACAAC AGACAAGTGT GCATTGACCC 300

130 GAAGCTAAAG TGGATTCAGG AGTACCTGGA GAAAGCTTTA AACAAGTAAG CACAACAGCC 360

131 AAAAAGGACT TTCCGCTAGA CCCACTCGAG GAAACTAAA ACCTTGTGAG AGATGAAAGG 420

132 GCAAAGACGT GGGGGAGGGG GCCTTAACCA TGAGGACCAG GTGTGTGTGT GGGGTGGGCA 480

133 CATTGATCTG GGATCGGGCC TGAGGTTTGC AGCATTTAGA CCCTGCATTT ATAGCATACG 540

134 GTATGATATT GCAGCTTATA TTCATCCATG CCCTGTACCT GTGCACGTTG GAACTTTTAT 600

135 TACTGGGGTT TTTCTTAGAA AGAAATTGTA TTATCAACAG CATTTTCAAG CAGTTAGTTC 660

136 CTTCATGATC ATCACAATCA TCATCATCTT CATTCTCATT TTTTAAATCA ACGAGTACTT 720

137 CAAGATCTGA ATTTGGCTTG TTTGGAGCAT CTCCTCTGCT CCCCTGGGGA GTCTGGGCAC 780

138 AGTCAGGTGG TGGCTTAACA GGGAGCTGGA AAAAGTGTC TTTCTTCAGA CACTGAGGCT 840

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153	CCCGCAGCAG	CGCCCCCTCCC	AAGAGGAAGG	CCTCTGTGGC	ACTCAGATAC	CGACTGGGGC	900
154							
155	TGGGGCGCCG	CCACTGCCTT	CACCTCCTCT	TTCAAACCTC	AGTGATTGGC	TCTGTGGGCT	960
156							
157	CCATGTAGAA	GCCACTATTA	CTGGGACTGT	CTCAGAGACC	CCTCTCCCAG	CTATTCCCTAC	1020
158							
159	TCTCTCCCCG	ACTCCGAGAG	CATGCTTAAT	CTTGCTTCTG	CTTCTCATTT	CTGTAGCCTG	1080
160							
161	ATCAGCGCCG	CACCAGCCGG	GAAGAGGGTG	ATTGCTGGGG	CTCGTGCCCT	GCATCCCTCT	1140
162							
163	CCTCCCAGGG	CCTGCCCCAC	AGCTCGGGCC	CTCTGTGAGA	TCCGTCTTTG	GCCTCCTCCA	1200
164							
165	GAATGGAGCT	GGCCCTCTCC	TGGGGATGTG	TAATGGTCCC	CCTGCTTACC	CGCAAAAGAC	1260
166							
167	AAGTCTTTAC	AGAATCAAAT	GCAATTTTAA	ATCTGAGAGC	TCGCTTGAGT	GACTGGGTTT	1320
168							
169	GTGATTGCCT	CTGAAGCCTA	TGTATGCCAT	GGAGGCACTA	ACAAACTCTG	AGGTTTCCGA	1380
170							
171	AATCAGAAGC	GAAAAAATCA	GTGAATAAAC	CATCATCTTG	CCACTACCCC	CTCCTGAAGC	1440
172							
173	CACAGCAGGG	GTTCAGGTTC	CAATCAGAAC	TGTTGGCAAG	GTGACATTTT	CATGCATAGA	1500
174							
175	TGCGATCCAC	AGAAGGTCCT	GGTGGTATTT	GTAACTTTTT	GCAAGGCATT	TTTTTATATA	1560
176							
177	TATTTTTGTG	CACATTTTTT	TTTACGATTC	TTTAGAAAAC	AAATGTATTT	CAAAATATAT	1620
178							
179	TTATAGTCGA	ACAAGTCATA	TATATGAATG	AGAGCCATAT	GAATGTCAGT	AGTTTATACT	1680
180							
181	TCTCTATTAT	CTCAAACTAC	TGGCAATTTG	TAAAGAAATA	TATATGATAT	ATAAATGTGA	1740
182							
183	TTGCAGCTTT	TCAATGTTAG	CCACAGTGTA	TTTTTTCACT	TGTACTAAAA	TTGTATCAAA	1800
184							
185	TGTGACATTA	TATGCACTAG	CAATAAAATG	CTAATTGTTT	CATGGTAAAA	AAAAAA	1856

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3526 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

201							
202	TCTCCGTCAG	CCGCATTGCC	CGCTCGGCGT	CCGGCCCCCG	ACCCGTGCTC	GTCCGCCCCG	60
203							
204	CCGCCCCGCC	GCCCGCGCCA	TGAACGCCAA	GGTCGTGGTC	GTGCTGGTCC	TCGTGCTGAC	120
205							

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206	CGCGCTCTGC CTCAGCGACG GGAAGCCCGT CAGCCTGAGC TACAGATGCC CATGCCGATT	180
207		
208	CTTCGAAAAGC CATGTTGCCA GAGCCAACGT CAAGCATCTC AAAATTCTCA ACACTCCAAA	240
209		
210	CTGTGCCCTT CAGATTGTAG CCCGGCTGAA GAACAACAAC AGACAAGTGT GCATTGACCC	300
211		
212	GAAGCTAAAG TGGATTCAAG AGTACCCTGA GAAAGCTTTA AACAAGAGGT TCAAGATGTG	360
213		
214	AGAGGGTCAC ACGCCTGAGG AACCCCTTACA GTAGGAGCCC AGCTCTGAAA CCAGTGTTAG	420
215		
216	GGAAGGGCCT GCCACAGCCT CCCCTGCCAG GGCAGCGCCC CAGGCATTGC CAAGGGCTTT	480
217		
218	GTTTTGCACA CTTTGCCATA TTTTCACCAT TTGATTATGT AGCAAAATAC ATGACATTTA	540
219		
220	TTTTTCATTT AGTTTGATTA TTCAGTGTCA CTGGCGACAC GTAGCAGCTT AGACTAAGGC	600
221		
222	CATTATTGTA CTTGCCTTAT TAGAGTGTCT TTCCACGGAG CCACTCCTCT GACTCAGGGC	660
223		
224	TCCTGGGTTT TGTATTCTCT GAGCTGTGCA GGTGGGGAGA CTGGGCTGAG GGAGCCTGGC	720
225		
226	CCCATGGTCA GCCCTAGGGT GGAGAGCCAC CAAGAGGGAC GCCTGGGGGT GCCAGGACCA	780
227		
228	GTCAACCTGG GCAAAGCCTA GTGAAGGCTT CTCTCTGTGG GATGGGATGG TGGAGGGCCA	840
229		
230	CATGGGAGGC TCACCCCTT CTCCATCCAC ATGGGAGCCG GGTCTGCCTC TTCTGGGAGG	900
231		
232	GCAGCAGGGC TACCCTGAGC TGAGGCAGCA GTGTGAGGCC AGGGCAGAGT GAGACCCAGC	960
233		
234	CCTCATCCCG AGCACCTCCA CATCCTCCAC GTTCTGCTCA TCATTCTCTG TCTCATCCAT	1020
235		
236	CATCATGTGT GTCCACGACT GTCTCCATGG CCCCACAAAA GGA CTCTCAG GACCAAAGCT	1080
237		
238	TTCATGTAAA CTGTGCACCA AGCAGGAAAT GAAAATGTCT TGTGTTACCT GAAAACACTG	1140
239		
240	TGCACATCTG TGTCTTGTGT GGAATATTGT CCATTGTCCA ATCCTATGTT TTTGTTCAAA	1200
241		
242	GCCAGCGTCC TCCTCTGTGA CCAATGTCTT GATGCATGCA CTGTTCCCCC TGTGCAGCCG	1260
243		
244	CTGAGCGAGG AGATGCTCCT TGGGCCCTTT GAGTGCAGTC CTGATCAGAG CCGTGGTCCT	1320
245		
246	TTGGGGTGAA CTACCTTGGT TCCCCACTG ATCACAAAAA CATGGTGGGT CCATGGGCAG	1380
247		
248	AGCCCAAGGG AATTCGGTGT GCACCAGGGT TGACCCAGA GGATTGCTGC CCCATCAGTG	1440
249		
250	CTCCCTCACA TGTCAGTACC TTCAAAC TAG GGCCAAGCCC AGCACTGCTT GAGGAAAACA	1500
251		
252	AGCATTCACA ACTTGTTTTT GGTTTTTAAA ACCCAGTCCA CAAAATAACC AATCCTGGAC	1560
253		
254	ATGAAGATTC TTTCCCAATT CACATCTAAC CTCATCTTCT TCACCATTG GCAATGCCAT	1620
255		
256	CATCTCCTGC CTTCTCCTG GGCCCTCTCT GCTCTGCGTG TCACCTGTGC TTCGGGCCCT	1680
257		
258	TCCCACAGGA CATTTCTCTA AGAGAACAAAT GTGCTATGTG AAGAGTAAGT CAACCTGCCT	1740

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**SEQUENCE VERIFICATION REPORT**  
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Original Text